UNIVERSITI TEKNOLOGI MARA

YAP (Y *ALU* POLYMORPHISM) SIGNATURE IN SIX MALAY SUB-ETHNIC GROUPS IN PENINSULAR MALAYSIA

MUHD. SHAH JEHAN
BIN ABD. RAZAK

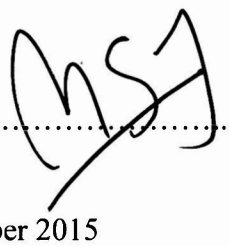
MSc

October 2015

AUTHOR'S DECLARATION

I declare that the work in this thesis/dissertation was carried out in accordance with the regulations of Universiti Teknologi Mara. It is original and is the result of my own work, unless otherwise indicated or acknowledged as referenced work. This thesis has not been submitted to any other academic institution or non-academic institution for any degree or qualification.

I, hereby, acknowledgment that I have been supplied with the Academic Rules and Regulations for Post Graduate, Universiti Teknologi Mara, regulating the conduct of my study and research.

Name of Student	:	Muhd. Shah Jehan Bin Abd. Razak
Student I.D. No.	:	2011441374
Programme	:	Master of Science (by Research)
Faculty	:	Applied Sciences
Dissertation Title	:	YAP (Y *Alu* Polymorphism) Signature in Six Malay Sub-Ethnic Groups in Peninsular Malaysia
Signature of Student	:	
Date	:	October 2015

ABSTRACT

Malay sub-ethnic groups in Peninsular Malaysia have a rich culture and tradition such as historical knowledge and heritage, which might be reflected in the current genetic makeup of this population. They are a mixture of different races that were caused by the history of migration centuries ago and consisted of 14 Malay sub-ethnic groups in Peninsular Malaysia. The objective of this study was to analyze the genetic polymorphism of Y chromosome at DYS287 Y *Alu* Polymorphism (YAP) locus in six Malay sub-ethnic groups of Peninsular Malaysia. A total of 231 buccal cells from healthy unrelated individual males consisting of 117 Kelantan-Malay, 50 Jawa-Malay, 48 Minangkabau-Malay, 9 Banjar Malay, 3 Bugis-Malay and 4 Rao-Malay from different regions of Peninsular Malaysia were screened for the DYS287 Y *Alu* locus from their genomic DNA. It shows that Kelantan-Malay, Jawa-Malay, Minangkabau-Malay, Banjar-Malay, Bugis-Malay and Rao-Malayare completely absent of theDYS287 Y *Alu* Polymorphism. Sequence results revealed that all Malay sub-ethnic of Peninsular Malaysia groups studied do not carry the number of 45bp (long) and 28bp (short) with association of long adenine (A)residues at [poly(A) tail] of the *Alu* sequence at DYS287 locus. Allele frequency for YAP+ was absent in all Malay sub-ethnic groups in Peninsular Malaysia. They were no genetic differences between the studied Malay sub-ethnic groups of DYS287 locus. This study has provided information on the pattern of DYS287 Y *Alu* Polymorphism in Kelantan-Malay, Jawa-Malay, Minangkabau-Malay, Banjar-Malay, Bugis-Malay and Rao-Malay sub-ethnic group in Peninsular Malaysia. Further study will be done on more samples of the other Malay sub-ethnic groups in Peninsular Malaysia to determine more DYS287 Y *Alu* Polymorphism status.

ACKNOWLEDGEMENT

In the name of ALLAH S.W.T, the Most Beneficial, the Most Merciful.

First of all, I would like to express my deep appreciation to my dear supervisor, Associate Professor Dr. Hajah Farida Zuraina Haji Mohd Yusof and Madam Wan Nurhayati Wan Hanafi for guiding and understanding me so well, providing me the ideas, comment, expertise, energy and time.

I would also like to give my gratitude to my lab-mates; Azzura Abdullah, Khairunisa Hassan and Sofia Sakina Mohd Yussup who always with me with their helpful ideas and support when I was dealing with problems in my research.

I am thankful to Mohd Faiz Ibrahim, Nor Hazwani Ghani, Nor Azhikin Zaini, Nor Fatihah Mohamed Razali, Mohd Maaruf Jaafar, Mohd Zakihalani A. Halim, Tuan Nor Azlin Tuan Aziz, Farah Naquiah Mohd Zaki, Tuan Haji Mohamed Harith Haji Zainal Abidin,Encik Masrol Selamat @ Hj. Sulaiman and Puan Ruslin Wahidun for their precious effort during samples collection. I would like to thank every volunteer to become the subjects without hesitating.

I wish to extend special thanks to Florinsiah Lorin, Farah Amna Othman, Nurul Husna Rosli and Ellia Kartini Mujar for their continuous support for me to write up my thesis, paper and slide.

Finally, I would like to extend my heartfelt gratitude to my parents; Abd.Razak Harun and Achon Abdul Kadir, my brother; Muhd. Shah Rizad, Muhd. Shah Nizam, Muhd. Azizu Hakim, Muhd. Azizi Azlan, and my best friends Mohd Shukri Harun and Raja Syawal Ehsan Raja Halid Shah for their patience, encourage and supporting.

Last but not least, I would like to thanks all my lecturer and my fellow friends who helped me out with the work during my study in this faculty.

This research was funded by Dana Kecemerlangan, 600-RMI/DANA 5/3/RIF (393/2012) from Universiti Teknologi Mara (UiTM).

MUHD. SHAH JEHAN BIN ABD. RAZAK

CHAPTER ONE
INTRODUCTION

1.1 BACKGROUND AND PROBLEM STATEMENT

Human Y chromosomehas been recognized as a useful marker for human population genetic studies (Ge, Budowle, Planz, Eisenberg, Ballantyne, and Chakraborty, 2010; Nadia, Pala, Battaglia, Grugni, Mohammed and Baharak, 2011; Primorac, Marjanoviç, Rudan, Viiems and Underhill, 2011). The non-recombining portion of human Y chromosomes has special features as a single haploid and involve only father to son transmission. As a consequence, the DNA sequence on the Y chromosome preserves a unique record of mutational events that occurred in previous generations. Therefore, polymorphisms in this region were proposed as tools for male-specific gene flow investigation and for reconstructing paternal history (Mizuno, Kitayama, Fujii, Nakahara, Yoshida and Sekiguchi, 2010). One of the most useful and widely studied wasthe Y-linked polymorphisms known as Y *Alu* Polymorphism (YAP) element. YAP element (DYS287 locus) is referred to the *Alu* insertion (~300bp) whichis present at a specific site on the long arm of the Y chromosome, Yq11 (Hammer, 1994).

This element is stable and originated almost 65 years ago as a component in human DNA (Tripathi, Cauhan, Tripathi and Agrawal, 2008). A DYS287 are basically referred to the acronym of YAP (Y*Alu* Polymorphism) and is basically generating biallelic polymorphism due to the absent or presence of the insertion. The YAP element are not present in all individual world population hence, a person can only carry either YAP+ or YAP- genotype meaning that carry insertion or a deletion (Ambrosio, Hernández, Novelletto, Dugoujon, Rodriguez and Cuesta, 2010). Analyses of YAP+ chromosome has been conducted in African, Tibetan and Japanese and has been proved to be useful in the evolutionary analysis of population studies (Vasudevan, Fatihah and Patimah, 2011). Besides that, studies have been conducted by Yang and colleagus 2008 between five ethnic groups from Northwest People Republic of China and were found at locus DYS287 Y *Alu* Polymorphismto be polymorphic. Thus, this type of marker can be shown to be a valuable for human population studies.